

1646

RAW SEQUENCE LISTING DATE: 11/24/2000
 PATENT APPLICATION: US/09/199,874C TIME: 14:59:48

Input Set : A:\Sequence.txt
 Output Set: N:\CRF3\11242000\I199874C.raw

ENTERED

Handwritten signature

4 <110> APPLICANT: Segre, Gino V.
 5 Kronenberg, Henry M.
 6 Abou-Samra, Abdul-Badi
 7 Juppner, Harald
 8 Potts, Jr., John T.
 9 Schipani, Ernestina
 11 <120> TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
 13 <130> FILE REFERENCE: 00786/071005
 15 <140> CURRENT APPLICATION NUMBER: US 09/199,874C
 16 <141> CURRENT FILING DATE: 1998-11-24
 18 <150> PRIOR APPLICATION NUMBER: US 08/471,494
 19 <151> PRIOR FILING DATE: 1995-06-06
 21 <160> NUMBER OF SEQ ID NOS: 28
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1862
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Didelphoidea
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (98)...(1642)
 34 <400> SEQUENCE: 1
 35 tgggcacagc caccctgttg gtagtcacagg ggccagcccca ctgagctggc atatacagctg 60
 36 gtggcccccgt tggactcggc cctaggggaac ggcggcg atg gga gcg ccc cgg atc 115
 37 Met Gly Ala Pro Arg Ile
 38 1 5
 40 tcg cac agc ctt gcc ttg ctc ctc tgc tgc tcc gtg ctc agc tcc gtc 163
 41 Ser His Ser Leu Ala Leu Leu Cys Cys Ser Val Leu Ser Ser Val
 42 10 15 20
 44 tac gca ctg gtg gat gcc gat gat gtc ata acg aag gag gag cag atc 211
 45 Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile
 46 25 30 35
 48 att ctt ctg cgc aat gcc cag gcc cag tgt gag cag cgc ctg aaa gag 259
 49 Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu
 50 40 45 50
 52 gtc ctc agg gtc cct gaa ctt gct gaa tct gcc aaa gac tgg atg tca 307
 53 Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser
 54 55 60 65 70
 56 agg tct gca aag aca aag aag gag aaa cct gca gaa aag ctt tat ccc 355
 57 Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro
 58 75 80 85
 60 cag gca gag gag tcc agg gaa gtt tct gac agg agc cgg ctg cag gat 403
 61 Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp
 62 90 95 100
 64 ggc ttc tgc cta cct gag tgg gac aac att gtg tgc tgg cct gct gga 451
 65 Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Ala Gly
 66 105 110 115

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DEC 11 2000

TECH CENTER 1000/2000

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68 gtg ccc ggc aag gtg gtg gcc gtg ccc tgc ccc gac tac ttc tac gac      499
69 Val Pro Gly Lys Val Val Ala Val Pro Cys Pro Asp Tyr Phe Tyr Asp
70      120      125      130
72 ttc aac cac aaa ggc cga gcc tat cgg cgc tgt gac agc aat ggc agc      547
73 Phe Asn His Lys Gly Arg Ala Tyr Arg Arg Cys Asp Ser Asn Gly Ser
74 135      140      145      150
76 tgg gag ctg gtg cct ggg aac aac cgg aca tgg gcg aat tac agc gaa      595
77 Trp Glu Leu Val Pro Gly Asn Asn Arg Thr Trp Ala Asn Tyr Ser Glu
78      155      160      165
80 tgt gtc aag ttt ctg acc aac gag acc cgg gaa cgg gaa gtc ttt gat      643
81 Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp
82      170      175      180
84 cgc ctc gga atg atc tac act gtg ggc tac tcc atc tct ctg ggc tcc      691
85 Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Ile Ser Leu Gly Ser
86      185      190      195
88 ctc act gtg gct gtg ctg att ctg ggt tac ttt agg agg tta cat tgc      739
89 Leu Thr Val Ala Val Leu Ile Leu Gly Tyr Phe Arg Arg Leu His Cys
90      200      205      210
92 acc cga aac tac att cac atg cat ctc ttc gtg tcc ttt atg ctc cgg      787
93 Thr Arg Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg
94 215      220      225      230
96 gct gta agc atc ttc atc aag gat gct gtg ctc tac tgc ggg gtt tcc      835
97 Ala Val Ser Ile Phe Ile Lys Asp Ala Val Leu Tyr Ser Gly Val Ser
98      235      240      245
100 aca gat gaa atc gag cgc atc acc gag gag gag ctg agg gcc ttc aca      883
101 Thr Asp Glu Ile Glu Arg Ile Thr Glu Glu Glu Leu Arg Ala Phe Thr
102      250      255      260
104 gag cct ccc cct gct gac aag gcg ggt ttt gtg ggc tgc aga gtg gcg      931
105 Glu Pro Pro Pro Ala Asp Lys Ala Gly Phe Val Gly Cys Arg Val Ala
106      265      270      275
108 gta acc gtc ttc ctt tac ttc ctg acc acc aac tac tac tgg atc ctg      979
109 Val Thr Val Phe Leu Tyr Phe Leu Thr Thr Asn Tyr Tyr Trp Ile Leu
110      280      285      290
112 gtg gaa ggc ctc tac ctt cac agc ctc atc ttc atg gct ttt ttc tct      1027
113 Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser
114 295      300      305      310
116 gag aaa aag tat ctc tgg ggt ttc aca tta ttt ggc tgg ggc ctc cct      1075
117 Glu Lys Lys Tyr Leu Trp Gly Phe Thr Leu Phe Gly Trp Gly Leu Pro
118      315      320      325
120 gcc gtg ttt gtc gct gtg tgg gtg acc gtg agg gct aca ctg gcc aac      1123
121 Ala Val Phe Val Ala Val Trp Val Thr Val Arg Ala Thr Leu Ala Asn
122      330      335      340
124 act gag tgc tgg gac ctg agt tgc ggg aat aag aaa tgg atc ata cag      1171
125 Thr Glu Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln
126      345      350      355
128 gtg ccc atc ctg gca gct att gtg gtg aac ttt att ctt ttt atc aat      1219
129 Val Pro Ile Leu Ala Ala Ile Val Val Asn Phe Ile Leu Phe Ile Asn
130      360      365      370
132 ata atc aga gtc ctg gct act aaa ctc cgg gag acc aat gca ggg aga      1267

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TECH CENTER 1600/2000

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Input Set : A:\Sequence.txt
 Output Set: N:\CRF3\11242000\I199874C.raw

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133 ile ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg
134 375 380 385 390
136 tgt gac acg agg caa caq tat aga aag ctg ctg aag tcc acg cta gtc 1315
137 Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val
138 395 400 405
140 ctc atg ccg cta ttt ggg gtg cac tac atc gtc ttc atg gcc acg ccg 1363
141 Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro
142 410 415 420
144 tac aca gaa gta tca ggg att ctt tgg caa gtc caa atg cac tat gaa 1411
145 Tyr Thr Glu Val Ser Gly Ile Leu Trp Gln Val Gln Met His Tyr Glu
146 425 430 435
148 atg ctc ttc aat tca ttc cag gga ttt ttc gtt gcc att ata tac tgt 1459
149 Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys
150 440 445 450
152 ttc tgc aat gga gag gta caa gca gag atc aag aag tca tgg agc cga 1507
153 Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg
154 455 460 465 470
156 tgg acc ctg gcc ttg gac ttc aag ccg aag gcc ccg agt ggc agc agt 1555
157 Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser
158 475 480 485
160 acc tac agc tat ggc ccc atg gtg tca cat aca agt gtc acc aat gtg 1603
161 Thr Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val
162 490 495 500
164 gga cct cga ggg ggc tgg cct tgt ccc tca gcc ctc gac tagctcctgg 1652
165 Gly Pro Arg Gly Gly Trp Pro Cys Pro Ser Ala Leu Asp
166 505 510 515
168 ggctggagcc agtgcgaatg gccatcacca gttgectggc tatgtgaagc atggttccat 1712
169 ttctgagaac tcattgcctt catctggccc agagcctggc accaaagatg acgggtatct 1772
170 caatggctct ggactttatg agccaatggt tggggaacag cccctccac tctggagga 1832
171 ggagagagag acagtcattgt gacccatatt 1862
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 1863
175 <212> TYPE: DNA
176 <213> ORGANISM: Didelphoidea
178 <220> FEATURE:
179 <221> NAME/KEY: CDS
180 <222> LOCATION: (98)...(1852)
182 <400> SEQUENCE: 2
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184 gtggccccgt tggactcggc cctaggggaa ggcggcg atg gga gcg ccc cgg atc 115
185 Met Gly Ala Pro Arg Ile
186 1 5
188 tgg cac agc ctt gcc ttg ctc ctc tgc tgc tcc gtg ctc agc tcc gtc 163
189 Ser His Ser Leu Ala Leu Leu Leu Cys Cys Ser Val Leu Ser Ser Val
190 10 15 20
192 tac gca ctg gtg gat gcc gat gat gtc ata acg aag gag gag cag atc 211
193 Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile
194 25 30 35
196 att ctt ctg cgc aat gcc cag gcc cag tgt gag cag cgc ctg aaa gag 259

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197	Ile	Leu	Leu	Arg	Asn	Ala	Gln	Ala	Gln	Cys	Glu	Gln	Arg	Leu	Lys	Glu	
198		40					45					50					
200	gtc	ctc	agg	gtc	cct	gaa	ctt	gct	gaa	tct	gcc	aaa	gac	tgg	atg	tca	307
201	Val	Leu	Arg	Val	Pro	Glu	Leu	Ala	Glu	Ser	Ala	Lys	Asp	Trp	Met	Ser	
202	55					60					65					70	
204	agg	tct	gca	aag	aca	aag	aag	gag	aaa	cct	gca	gaa	aag	ctt	tat	ccc	355
205	Arg	Ser	Ala	Lys	Thr	Lys	Lys	Glu	Lys	Pro	Ala	Glu	Lys	Leu	Tyr	Pro	
206					75					80						85	
208	cag	gca	gag	gag	tcc	agg	gaa	gtt	tct	gac	agg	agc	cgg	ctg	cag	gat	403
209	Gln	Ala	Glu	Glu	Ser	Arg	Glu	Val	Ser	Asp	Arg	Ser	Arg	Leu	Gln	Asp	
210			90						95					100			
212	ggc	ttc	tgc	cta	cct	gag	tgg	gac	aac	att	gtg	tgc	tgg	cct	gct	gga	451
213	Gly	Phe	Cys	Leu	Pro	Glu	Trp	Asp	Asn	Ile	Val	Cys	Trp	Pro	Ala	Gly	
214			105						110					115			
216	gtg	ccc	ggc	aag	gtg	gtg	gcc	gtg	ccc	tgc	ccc	gac	tac	ttc	tac	gac	499
217	Val	Pro	Gly	Lys	Val	Val	Ala	Val	Pro	Cys	Pro	Asp	Tyr	Phe	Tyr	Asp	
218		120					125					130					
220	ttc	aac	cac	aaa	ggc	cga	gcc	tat	cgg	cgc	tgt	gac	agc	aat	ggc	agc	547
221	Phe	Asn	His	Lys	Gly	Arg	Ala	Tyr	Arg	Arg	Cys	Asp	Ser	Asn	Gly	Ser	
222	135					140					145				150		
224	tgg	gag	ctg	gtg	cct	ggg	aac	aac	cgg	aca	tgg	gcg	aat	tac	agc	gaa	595
225	Trp	Glu	Leu	Val	Pro	Gly	Asn	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	
226					155					160					165		
228	tgt	gtc	aag	ttt	ctg	acc	aac	gag	acc	cgg	gaa	cgg	gaa	gtc	ttt	gat	643
229	Cys	Val	Lys	Phe	Leu	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	
230				170					175					180			
232	cgc	ctc	gga	atg	atc	tac	act	gtg	ggc	tac	tcc	atc	tct	ctg	ggc	tcc	691
233	Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Ile	Ser	Leu	Gly	Ser	
234		185					190					195					
236	ctc	act	gtg	gct	gtg	ctg	att	ctg	ggt	tac	ttt	agg	agg	tta	cat	tgc	739
237	Leu	Thr	Val	Ala	Val	Leu	Ile	Leu	Gly	Tyr	Phe	Arg	Arg	Leu	His	Cys	
238		200					205					210					
240	acc	cga	aac	tac	att	cac	atg	cat	ctc	ttc	gtg	tcc	ttt	atg	ctc	cgg	787
241	Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	
242	215					220					225				230		
244	gct	gta	agc	atc	ttc	atc	aag	gat	gct	gtg	ctc	tac	tgc	ggg	gtt	tcc	835
245	Ala	Val	Ser	Ile	Phe	Ile	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Val	Ser	
246				235						240				245			
248	aca	gat	gaa	atc	gag	cgc	atc	acc	gag	gag	gag	ctg	agg	gcc	ttc	aca	883
249	Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu	Glu	Leu	Arg	Ala	Phe	Thr	
250			250						255					260			
252	gag	cct	ccc	cct	gct	gac	aag	gcg	ggt	ttt	gtg	ggc	tgc	aga	gtg	gcg	931
253	Glu	Pro	Pro	Pro	Ala	Asp	Lys	Ala	Gly	Phe	Val	Gly	Cys	Arg	Val	Ala	
254			265						270					275			
256	gta	acc	gtc	ttc	ctt	tac	ttc	ctg	acc	acc	aac	tac	tac	tgg	atc	ctg	979
257	Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	
258		280					285						290				
260	gtg	gaa	ggc	ctc	tac	ctt	cac	agc	ctc	atc	ttc	atg	gct	ttt	ttc	tct	1027
261	Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	

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262	295		300		305		310	
264	gag	aaa	aag	tat	ctc	tgg	ggt	ttc
265	Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe
266								
268	gcc	gtg	ttt	gtc	gct	gtg	tgg	gtg
269	Ala	Val	Phe	Val	Ala	Val	Trp	Val
270								
272	act	gag	tgc	tgg	gac	ctg	agt	tcg
273	Thr	Glu	Cys	Trp	Asp	Leu	Ser	Ser
274								
276	gtg	ccc	atc	ctg	gca	gct	att	gtg
277	Val	Pro	Ile	Leu	Ala	Ala	Ile	Val
278								
280	ata	atc	aga	gtc	ctg	gct	act	aaa
281	Ile	Ile	Arg	Val	Leu	Ala	Thr	Lys
282								
284	tgt	gac	acg	agg	caa	cag	tat	aga
285	Cys	Asp	Thr	Arg	Gln	Gln	Tyr	Arg
286								
288	ctc	atg	ccg	cta	ttt	ggg	gtg	cac
289	Leu	Met	Pro	Leu	Phe	Gly	Val	His
290								
292	tac	aca	gaa	gta	tca	ggg	att	ctt
293	Tyr	Thr	Glu	Val	Ser	Gly	Ile	Leu
294								
296	atg	ctc	ttc	aat	tca	ttc	cag	gga
297	Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly
298								
300	ttc	tgc	aat	gga	gag	gta	caa	gca
301	Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala
302								
304	tgg	acc	ctg	gcc	ttg	gac	ttc	aag
305	Trp	Thr	Leu	Ala	Leu	Asp	Phe	Lys
306								
308	acc	tac	agc	tat	ggc	ccc	atg	gtg
309	Thr	Tyr	Ser	Tyr	Gly	Pro	Met	Val
310								
312	gga	cct	cga	ggg	ggg	ctg	gcc	ttg
313	Gly	Pro	Arg	Gly	Gly	Leu	Ala	Leu
314								
316	ggg	gct	gga	gcc	agt	gcc	aat	ggc
317	Gly	Ala	Gly	Ala	Ser	Ala	Asn	Gly
318								
320	aag	cat	ggg	tcc	att	tct	gag	aac
321	Lys	His	Gly	Ser	Ile	Ser	Glu	Asn
322								
324	cct	ggc	acc	aaa	gat	gac	ggg	tat
325	Pro	Gly	Thr	Lys	Asp	Asp	Gly	Tyr
326								

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L:724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8